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Scientific and Technical Information Center

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Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Point of Contact:

Jan Delaval
Librarian-Physical Sciences
CM1-TE01 Tel: 308-4498**STAFF USE ONLY**Searcher: JanSearcher Phone #: 4498Searcher Location: Room 2205Date Searcher Picked Up: 12/18Date Completed: 12/18

Searcher Prep & Review Time: _____

Clerical Prep Time: 10Online Time: 10**Type of Search**

NA Sequence (#) _____

AA Sequence (#) ✓

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

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Sequence Systems ✓

WWW/Internet _____

Other (specify) _____

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OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 12.49 seconds
(without alignments)
1118.439 Million cell updates/sec

Title: US-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLLAILFCALWSAVLAENS.....NIVGWGVTQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
al number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	2007	100.0	381	1 PTX3_HUMAN	P26022 homo sapien
2	1667	83.1	381	1 PTX3_MOUSE	P48759 mus musculus
3	296.5	14.8	427	1 APEX_CAVPO	P47970 cavia porce
4	295.5	14.7	430	1 NPX2_HUMAN	P47972 homo sapien
5	289	14.4	432	1 NPX1_RAT	P47971 rattus norv
6	287	14.3	432	1 NPX1_MOUSE	Q62443 mus musculus
7	281	14.0	430	1 NPX1_HUMAN	Q15818 homo sapien
8	256.5	12.8	242	1 CRP4_LIMPO	P06206 limulus pol
9	249.5	12.4	242	1 CRP3_LIMPO	P06207 limulus pol
10	248.5	12.4	242	1 CRP1_LIMPO	P06205 limulus pol
11	225.5	11.2	230	1 CRP_RAT	P48199 rattus norv
12	218.5	10.9	416	1 PXN1_XENLA	P49263 xenopus lae
13	217.5	10.8	225	1 CRP_MESAU	P49262 mesocricetu
14	212.5	10.6	231	1 FP_CRIMI	P15697 cricetus
15	203.5	10.1	225	1 CRP_MOUSE	P14847 mus musculus
16	199.5	9.9	225	1 CRP_RABIT	P02742 oryctolagus
17	192.5	9.6	234	1 CRP_CAVPO	P49254 cavia porce
18	187.5	9.3	234	1 SAMP_MESAU	P07629 mesocricetu
19	184.5	9.2	224	1 CRP_HUMAN	P02741 homo sapien
20	181	9.0	238	1 CRP_XENLA	Q07203 xenopus lae
21	179.5	8.9	228	1 SAMP_RAT	P23680 rattus norv
22	166	8.3	224	1 SAMP_MOUSE	P12246 mus musculus
23	164.5	8.2	223	1 SAMP_CAVPO	P49255 cavia porce
24	161.5	8.0	223	1 SAMP_HUMAN	P02743 homo sapien
25	112.5	5.6	899	1 PR06_YEAST	P19735 saccharomyc
26	99.5	5.0	651	1 PRIA_MYCLE	Q9ccc3 mycobacteri
27	99	4.9	304	1 MMGL_MOUSE	P49300 mus musculus
28	97.5	4.9	412	1 NEMO_MOUSE	O88522 m nf-kappab
29	97	4.8	1170	1 XPG_MOUSE	P35689 mus musculus
30	95	4.7	284	1 TPM1_BIOGL	P42636 biomphalari
31	94	4.7	527	1 HSF8_LYCES	Q40152 lycopersico
32	92.5	4.6	284	1 TPM2_BIOGL	P43689 biomphalari
33	92	4.6	306	1 MMGL_RAT	P49301 rattus norv

ALIGNMENTS

RESULT 1

PTX3_HUMAN
ID PTX3_HUMAN STANDARD: PRT; 381 AA.
AC P26022;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-
DE INDUCIBLE PROTEIN TSG-14).
GN PTX3 OR TSG14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=93054498; PubMed=1429570;
RA Breviario F., D'Aniello E.M., Golay J., Peri G., Bottazi B.,
RA Bairoch A., Saccone S., Marzella R., Predazzi V., Rocchi M.,
RA della Valle G., Dejana E., Mantovani A., Introna M.; Cloning of a new
RT interleukin-1-inducible genes in endothelial cells. Cloning of a new
RT gene related to C-reactive protein and serum amyloid P component.;"
RL J. Biol. Chem. 267:22190-22197(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=94178310; PubMed=8131794;
RA Introna M., Breviario F., D'Aniello E.M., Golay J., Dejana E.,
RA Mantovani A.;
RT "IL-1 inducible genes in human umbilical vein endothelial cells.;"
RL Eur. Heart J. 14:78-81(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fore skin;
RX MEDLINE=93171605; PubMed=7679696;
RA Lee G.W., Lee T.H., Vilcek J.;
RT "TSG-14, a tumor necrosis factor- and IL-1-inducible protein, is a
RT novel member of the pentaxin family of acute phase proteins.;"
RL J. Immunol. 150:1804-1812(1993).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=95015860; PubMed=7523502;
RA Lee G.W., Goodman A.R., Lee T.H., Vilcek J.;
RT "Relationship of TSG-14 protein to the pentaxin family of major
RT acute phase proteins.;"
RL J. Immunol. 153:3700-3707(1994).
CC -I- INDUCTION: BY INTERLEUKIN-1 BETA AND TNF-ALPHA.
CC -I- PTM: GLYCOSYLATED (PROBABLE).
CC -I- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
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34 92 4.6 866 1 NASA_KLEPN Q05457 klebsiella
35 92 4.6 958 1 VIA_CCMV P27752 cowpea chlo
36 91.5 4.6 230 1 Y966_MYCTU P71544 mycobacteri
37 91.5 4.6 280 1 ST02_CAEEL Q19958 caenorhabd
38 91 4.5 864 1 AKA3_MOUSE O88987 mus musculu
39 90.5 4.5 527 1 HSF8_LYCPD P41153 lycopersico
40 90.5 4.5 1969 1 MYSA_CAEEL P12844 caenorhabd
41 90.5 4.5 2035 1 EVPL_MOUSE Q9d952 mus musculu
42 90.5 4.5 5430 1 ACF7_HUMAN Q9upn3 homo sapien
43 90 4.5 283 1 LECH_RAT P02706 rattus norv
44 90 4.5 330 1 Y677_METJA Q58090 methanococc
45 89.5 4.5 1487 1 ICP4_HSVK P17473 equine herp

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CC EMBL; X63053; CAA44778.1; -
 CC EMBL; X63613; CAA45158.1; -
 CC EMBL; M31166; AAA61234.1; -
 CC PIR; S18947; S18947.
 CC PIR; S17069; S17069.
 CC PIR; A44323; A44323.
 CC MIM; 602492; -
 CC InterPro; IPR001759; Pentaxin.
 CC Pfam; PF00354; pentaxin; 1.
 CC PRINTS; PR00895; PENTAXIN.
 CC SMART; SM00159; PTX; 1.
 CC PROSITE; PS00289; PENTAXIN; 1.
 CC Pentaxin; Glycoprotein; Signal.
 CC SIGNAL 1 17 POTENTIAL.
 CC CHAIN 18 381 PENTAXIN-RELATED PROTEIN PTX3.
 CC DOMAIN 183 381 PENTAXIN.
 CC DISULFID 210 271 BY SIMILARITY.
 CC CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 202 202 M -> L (IN REF. 3).
 CC SEQUENCE 381 AA; 42019 MW; 787F749DBC6D59B CRC64;

Query Match 100.0%; Score 2007; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3.1e-148;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHLAIFCALWSAVLAENSDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
 DB 1 MHLAIFCALWSAVLAENSDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
 QY 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTSALDEL 120
 DB 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTSALDEL 120
 QY 121 LOATRDAGRRLARMEGAEOPEEAGRALAAVLEELQRTADLHAGVQWAARSWLPAGCE 180
 DB 121 LOATRDAGRRLARMEGAEOPEEAGRALAAVLEELQRTADLHAGVQWAARSWLPAGCE 180
 QY 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVNLKTLFSGYGRNPEYIQLYL 240
 DB 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVNLKTLFSGYGRNPEYIQLYL 240
 QY 241 SYQSIIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
 DB 241 SYQSIIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
 QY 301 IVPEGGTLOIGQKNGCCVGGGDETLAFSGRLTGNIWDSVLSNBEIRETGGAESCHIR 360
 DB 301 IVPEGGTLOIGQKNGCCVGGGDETLAFSGRLTGNIWDSVLSNBEIRETGGAESCHIR 360
 QY 361 GNIVGSGVTEIPIHGGAQYVS 381
 DB 361 GNIVGSGVTEIPIHGGAQYVS 381

RESULT 2
 PTX3_MOUSE
 ID PTX3_MOUSE STANDARD; PRT; 381 AA.
 AC P48759;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-
 DE INDUCIBLE PROTEIN TSG-14).
 GN PTX3 OR TSG14.
 QS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57; TISSUE=Fibroblast;
 RX MEDLINE=96202510; PubMed=8634434;
 RA Introna M., Vidal Alles V., Castellano M., Picardi G., de Gioia L.,
 RA Bottazzal B., Peri G., Breviaro F., Salmona M., de Gregorio I.,
 RA Dragani T.A., Srinivasan N., Blundell T.L., Hamilton T.A.,
 RA Mantovani A.;
 RT "Cloning of mouse ptx3, a new member of the pentraxin gene family
 RT expressed at extrahepatic sites.";
 RL Blood 87:1862-1872(1996).
 RN [2]
 RP SEQUENCE OF 1-177 FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96029644; PubMed=7592730;
 RA Altmeyer A., Klampfer L., Goodman A.R., Vilcek J.;
 RT "Promoter structure and transcriptional activation of the murine
 RT TSG-14 gene encoding a tumor necrosis factor/interleukin-1-inducible
 RT pentraxin protein.";
 RL J. Biol. Chem. 270:25584-25590(1995).
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
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EMBL; X83601; CAA58580.1; -
 EMBL; U33842; AAC52273.1; -
 MGD; MGI:104641; Ptx3.
 InterPro; IPR001759; Pentaxin.
 Pfam; PF00354; pentaxin; 1.
 PRINTS; PR00895; PENTAXIN.
 SMART; SM00159; PTX; 1.
 PROSITE; PS00289; PENTAXIN; 1.
 Pentaxin; Glycoprotein; Signal.
 SIGNAL 1 17 POTENTIAL.
 CHAIN 18 381 PENTAXIN-RELATED PROTEIN PTX3.
 DOMAIN 183 381 PENTAXIN.
 DISULFID 210 271 BY SIMILARITY.
 CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CONFLICT 50 50 R -> A (IN REF. 2).
 CONFLICT 90 90 A -> S (IN REF. 2).
 CONFLICT 161 161 A -> S (IN REF. 2).
 CONFLICT 172 172 R -> H (IN REF. 2).
 SEQUENCE 381 AA; 41811 MW; E3CA3B1D93CFE4EB CRC64;

Query Match 83.1%; Score 1667; DB 1; Length 381;
 Best Local Similarity 82.2%; Pred. No. 6.5e-122;
 Matches 313; Conservative 22; Mismatches 46; Indels 0; Gaps 0;

QY 1 MHLAIFCALWSAVLAENSDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
 DB 1 MHLAIFCALWSAVVAETSDDYELMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
 QY 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTSALDEL 120
 DB 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAGGAPADARLVRLEPL 120
 QY 121 LOATRDAGRRLARMEGAEOPEEAGRALAAVLEELQRTADLHAGVQWAARSWLPAGCE 180
 DB 121 LOESRDASRLARLEDAEARREPEATVPGLGAVLEELRRTRADLSAVQSVWARHWPAGCE 180
 QY 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVNLKTLFSGYGRNPEYIQLYL 240
 DB 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVNLKTLFSGYGRNPEYIQLYL 240
 QY 241 SYQSIIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
 DB 241 SSQSLVVLVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300

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QY 301 IYPEGILQIGOEKNGCCVGGGDETLAFSGRLTGFTNWDVSLNEEIRETGARSCHIR 360
DB 301 SYPEGGLQIGOEKNGCCVGGGDESLAFSGRLTGFTNWDVSLNEEIRASGVESCHIR 360
QY 361 GNIVGVGTETIOPHGAQYVS 381
DB 361 GNIVGVGTETIOPHGAQYVS 381

RESULT 3
APEX_CAVPO STANDARD; PRT: 427 AA.
AC P47970;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE APEXIN PRECURSOR (ACROSOMAL PENTAXIN-LIKE PROTEIN P50) (AM50).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathia; Caviidae; Cavia.
NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 223-227; 328-337 AND 342-377.
RC STRAIN-HARTLEY; TISSUE-Testis;
RX MEDLINE=95096119; PubMed=7798265;
RA Noland T.D., Friday B.B., Maulit M.T., Gerton G.L.;
RT "The sperm acrosomal matrix contains a novel member of the pentaxin
family of calcium-dependent binding proteins.";
RL J. Biol. Chem. 269:32607-32614(1994).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 254-279; 316-330 & 359-389.
RC STRAIN-HARTLEY; TISSUE-Testis;
RX MEDLINE=95096120; PubMed=7798266;
RA Reid M.S., Blobel C.P.;
RT "Apexin, an acrosomal pentaxin.";
RL J. Biol. Chem. 269:32615-32620(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN BINDING, CONCENTRATING, AND SORTING
SOLUBLE GLYCOPROTEINS OR GLYCOLIPIDS THAT ARE DESTINED FOR THE
ACROSOME.
CC -!- SUBUNIT: OLIGOMERIC; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SPERM ACROSOMAL MATRIX.
CC -!- TISSUE SPECIFICITY: TESTIS SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
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CC -----
CC EMBL: U13234; AAA64994.1; -.
DR EMBL: U13236; AAA64995.1; -.
DR HSP: P06205; LLIM.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin; 1.
DR PRINTS: PR00895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTAXIN; 1.
KW Pentaxin; Sperm; Glycoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 427 APEXIN.
FT DOMAIN 223 427 PENTAXIN.
FT DISULFD 249 309 BY SIMILARITY.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 140 141 MISSING (IN REF. 2).
FT CONFLICT 279 279 E -> S (IN REF. 2; AA SEQUENCE).
FT CONFLICT 329 329 G -> S (IN REF. 2; AA SEQUENCE).
SQ SEQUENCE 427 AA; 47233 MW; D24F8F07A89E09A CRC64;

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Query Match 14.8%; Score 296.5; DB 1; Length 427;
Best Local Similarity 24.5%; Pred. No. 1e-15;
Matches 94; Conservative 60; Mismatches 121; Indels 109; Gaps 14;

QY 67 QMRERMLQ-----ATDDVLRGELORLREELG-----RLAESLA 100
DB 65 QURETVVMQKETLGAOREAIRELTSLKARCEGLMAGKAESKDTGDLPRDPSRVVEQLS 124
QY 101 RPCA-----PGAPAEAR--LTSALDELLOATRDAGRRLARME--- 135
DB 125 RSLQVLKDRLESLQLRTNASNTGLPSPDFREVLRRLGEL---ERQLLRKVAELEDERS 181
QY 136 -----GAEAPQPEPAGRALAAVLEELROTADLHVAQVGAARSWLPACETAILEPMS 189
DB 182 LLHNETSAAHQKTENTLALLQRTVTELEGRNSAFKSPDAF-----KVSLPFRT 229
QY 190 KFIQSVHVPVRMRLESFSAACVWKAT-----DVLNKTILFSYCTKKNPYE 235
DB 230 NYLYGKIKKTLF-ELYSFYICLWLRSSASPGIGTSPSYAVPGQANEIVLIEWG--NNPIE 286
QY 236 IOLYLSYQISQIVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSSEGLTSLWVNGELAAIT 293
DB 287 LLI-----NDKVAQLPLFVSDGKWHHICITWTTRDGLWEAFQDGEKLG 331
QY 294 VEMATGHIVPEGGILQIGOEKNGCCVGGGDETLAFSGRLTGFTNWDVSLNEEIRETG 353
DB 332 ENLAWHPRIKSGVLLILGQEQD--TVGGRFDATQAPVGLSOFNIWDRVLRQPEISNIAN 389
QY 354 AESCHIRGNIVGWVTEIOPHGA 377
DB 390 C-SLMAGNIIPWVDNNVDVFGGA 412

RESULT 4
NPX2_HUMAN
ID NPX2_HUMAN STANDARD; PRT: 430 AA.
AC P47972;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEURONAL PENTAXIN II PRECURSOR (NP-II) (NP2).
GN NPX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96015050; PubMed=8530029;
RA Hsu Y.-C., Perin M.S.;
RT "Human neuronal pentaxin II (NPX2): conservation, genomic
structure, and chromosomal localization.";
RL Genomics 28:220-227(1995).
CC -!- SUBCELLULAR LOCATION: SECRETORY VESICLES (POTENTIAL).
CC -!- TISSUE SPECIFICITY: BRAIN, PANCREAS, LIVER, HEART, AND SKELETAL
MUSCLE. HIGHEST LEVELS ARE SEEN IN THE TESTIS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
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CC -----
CC EMBL: U29195; AAA68980.2; -.
DR EMBL: U29191; AAA68980.2; JOINED.
DR EMBL: U29192; AAA68980.2; JOINED.
DR EMBL: U29193; AAA68980.2; JOINED.

```

THE NEURONAL AND GLIAL UPTAKE OF THE SNAKE VENOM TOXIN TAIPOXIN.
 -!- SUBCELLULAR LOCATION: SECRETORY VESICLES (POTENTIAL).
 -!- TISSUE SPECIFICITY: CEREBELLUM, HIPPOCAMPUS and CEREBRAL CORTEX.
 -!- PTM: GLYCOSYLATED.
 -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.

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 EMBL; U18772; AAA92685.1; -
 HSP; P06205; LIIM
 InterPro; IPR001759; Pentaxin.
 Pfam; PF00354; pentaxin; 1.
 PRINTS; PR00895; PENTAXIN.
 SMART; SM00159; PTX; 1.
 PROSITE; PS00289; PENTAXIN; 1.
 Pentaxin; Signal; Glycoprotein.
 SIGNAL 1 17 POTENTIAL.
 CHAIN 18 432 NEURONAL PENTRAXIN I.
 DOMAIN 230 432 PENTAXIN.
 DISULFID 256 316 BY SIMILARITY.
 CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 432 AA; 47216 MW; 3071E3E40ACA3820 CRC64;

Query Match 14.4%; Score 289; DB 1; Length 432;
Best Local Similarity 24.2%; Pred. NO. 4e-15;
Matches 93; Conservative 61; Mismatches 134; Indels 96; Gaps 13;

67 QMRERMLQATDDVLERGE-LQRLREELGRLAESLARPCAPG----- 106

```
Dbb      |||::|||:::||::|||::|||
60 QLRETVLQKETILSQKETIRELTIKLCRCESQSTLDAGPGEARRSGGRKPQGSGKNMG 119
```

20Y 107 ----APAEARL-----TSAIDELJOATRDAGR--LA 132

db 120 DLSRTPASETILSOLGOTLOSITRIENI FOVSPI NSSCSOTNCSI KOT LOSKTRDTPRPAHUS 170

09 133 RM-----ECAPACDDEEACDA-I AAIIT NPI POTPAATVHICOGI...TOWR-C-
.....S...C...Q...Z...Q...K...INENWUQISRENSSOQINSUNDETQSRIIDUEQRQVLS I79

[illegible]

180 RVNTLEEGRGPKNDDTEERAKIESALTSLHQRISELEKGQ----KDNRP-GDKFQLTFPL 234

188 RSKKIFGSVHPVRPMRLEFSACIWKATDV-----LNKTI LFSYGTKRNP 233

235 RTNMYAKVKKSLP-EMYAFVCMWLKSSAAPGVGTFPSYAVPGQANELVLEWG--NNP 291

234 YEIQLYLSYQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTSLWVNGELAATT 293

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bb      || :       : ||:          | : | : | : | : | : | : |
292 MEILINDKVAKLPEVIND-----GKWHHCIVTWTTRDGVWEAYODSTOGANG 338
```

294 VEMATCHIVPEGGILOIGOEKNGCCVGGGDETTAFSGPITCENIWDSVI SNEETIDMCC 252

[illegible]

353 ENRHH LNF INFQGV LV LGQEQD - ILGGGFDAIQA FVGEAHFNINDRKLTPGEVYNLAT 396

334 AESCHIRGNIVGWSYTEIQPHGGA 377

397 CSSKALSGNVIWAESQIEIFGGA 420

RESULT 6

NPX1_MOUSE	432
D NPX1_MOUSE	432
STANDARD.	432

Q62443; FRI; 432 AA.
 REAT_MOUSE STANDARD; FRI; 432 AA.
 01 NOV 1997 12:25

T 01-NOV-1997 (Rel. 35, Created)

T 01-NOV-1997 (Rel. 35, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)
NEURONAL PENTAXIN I PRECURSOR (NP-I) (NP1)

N NPTX1.

QY 188 RSKKIFGSHVPRMRLSEFSACIWKATDV-----LNKTLIFSCTKRNK 233
 Db 233 RTNYMYAKVKSLLP-EMVAFVCMWLKSSATPGVGTPEFSAVPGQANLVLIENG--NNP 289
 QY 234 YEQLYLSVQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSSEGLTSLWVNGELAATT 293
 Db 290 MEILLNDKVKLPFFVIND-----GKWHICVITWTTRDGVWVEAYQDGTQGGSG 336
 QY 294 VEMATGHIPEGGIILQIGOEKNGCCVGGFDETLAFSGRLTGFNWDSVLSNEEIRETGG 353
 Db 337 ENLAFYHPKIPQGLVVGQEQD--TLGGGFDAFQAFGELAHFNWDRKRLTPGVEYNLAT 394
 QY 354 AESCHIRGNIVGWGTEIQPHGGA 377
 Db 395 CSTKALSGNVIAWAEASHIEIYCGA 418

RESULT 8
 CRP4_LIMPO STANDARD; PRT; 242 AA.
 P06206;
 01-JAN-1988 (Rel. 06, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 01-FEB-1996 (Rel. 33, Last annotation update)
 DE C-REACTIVE PROTEIN 1.4 PRECURSOR.
 OS Limulus polyphemus (Atlantic horseshoe crab).
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Limulus.
 OX NCBI_TaxID=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86278105; PubMed=3015932;
 RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
 RT "Isolation and characterization of Limulus C-reactive protein genes.";
 RL J. Biol. Chem. 261:10450-10455(1986).
 RN [2]
 RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=86278106; PubMed=2426265;
 RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
 RT "The amino acid sequence of Limulus C-reactive protein. Evidence of
 polymorphism.";
 RL J. Biol. Chem. 261:10456-10465(1986).
 CC -!- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; M14024; AAA28268.1; -
 CC PIR; A25192; A25192.
 CC PIR; A25193; A25193.
 CC HSP; P06205; ILM.
 CC InterPro; IPR001759; Pentaxin.
 CC Pfam; PF00354; pentaxin.1.
 CC PRINTS; PR00895; PENTAXIN.
 CC SMART; SM00159; PTX; 1.
 CC PROSITE; PS00289; PENTAXIN; 1.
 CC Pentaxin; Calcium; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 242 C-REACTIVE PROTEIN 1.4.
 FT DOMAIN 25 242 PENTAXIN.
 FT DISULFID 62 125
 FT DISULFID 112 144
 FT DISULFID 207 241
 FT CARBOHYD 147 147
 FT DOMAIN 52 67 N-LINKED (GLCNAC...).
 BINDING OF PHOSPHORYLCHOLINE (POTENTIAL).

FT DOMAIN 59 60 INTERACTION WITH PHOSPHATE GROUP OF
 FT BINDING 63 63 PHOSPHORYLCHOLINE (POTENTIAL).
 FT QUATERNARY AMMONIUM GROUP OF
 FT PHOSPHORYLCHOLINE (POTENTIAL).
 FT SIMILAR 139 153 STRONG WITH CA-BINDING EF-HAND SEQUENCE.
 SQ SEQUENCE 242 AA; 26842 MW; EEC7AC5B47E76459 CRC64;
 Query Match 12.8%; Score 256.5; DB 1; Length 242;
 Best local Similarity 29.4%; Pred. No. 6.3e-13;
 Matches 60; Conservative 42; Mismatches 87; Indels 15; Gaps 6;
 QY 183 ILFPMRSKIFGSHVPRM-RLESEFACIWKATDVLNKTLIFSCTKRNKPYEQLYLS 241
 Db 34 VKFPPSSPFPRLVMTPLDQETLCYFKNVHLKSTLTIFSYTAKNDNELLTSL 93
 QY 242 YQSI--VFVVGGEENKLVAEAMVSLGRWTHLCGTWNSSEGLTSLWVNG-ELAATTVMAT 298
 Db 94 KQGAFAHNVHGAPOKVKQCPNKTHIGKWHVCHTWSSWEGEATIGVDGFCHKGNATGAM 153
 QY 299 GHIVPEGGIILQIGOEKNGCCVGGFDETLAFSGRLTGFNWDSVLSNEEIRETGGAES 357
 Db 154 GVTLSQGLVVGQEQDS--VGGEYDAEQLSELSLNLWNTVNLNHEQIKH---LSKCA 208
 QY 358 -----HIRGNIVGWGTEIQPHGG 376
 Db 209 HPSERHIGHNIQWDTQFCAYDG 232

RESULT 9
 CRP3_LIMPO STANDARD; PRT; 242 AA.
 AC P06207;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE C-REACTIVE PROTEIN 3.3 PRECURSOR.
 OS Limulus polyphemus (Atlantic horseshoe crab).
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Limulus.
 OX NCBI_TaxID=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86278105; PubMed=3015932;
 RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
 RT "Isolation and characterization of Limulus C-reactive protein genes.";
 RL J. Biol. Chem. 261:10450-10455(1986).
 RN [2]
 RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=86278106; PubMed=2426265;
 RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
 RT "The amino acid sequence of Limulus C-reactive protein. Evidence of
 polymorphism.";
 RL J. Biol. Chem. 261:10456-10465(1986).
 CC -!- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; M14025; AAA28269.1; -
 CC PIR; B25192; B25192.
 CC PIR; B25193; B25193.
 CC HSP; P06205; ILM.
 CC InterPro; IPR001759; Pentaxin.
 CC Pfam; PF00354; pentaxin.1.


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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RC MEDLINE=92147634; PubMed=1737750;
RA Rassouli M., Sambasivam H., Azadi P., Dell A., Morris H.R.,
RA Nagpurkar A., Mookerjee S., Murray P.R.K.;
RT "Derivation of the amino acid sequence of rat C-reactive protein from
RT cDNA cloning with additional studies on the nature of its dimeric
RT component.";
RL J. Biol. Chem. 267:2947-2954(1992).
CC -|- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST
CC PHAGOCYTOSIS. IT PROMOTES AGGLUTINATION, BACTERIAL CAPSULAR SWELLING,
CC PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT
CC BINDING TO PHOSPHORYLCHOLINE. IN CONTRAST TO HUMAN CRP, IT BINDS
CC 3 MOLECULES OF PHOSPHORYLCHOLINE INSTEAD OF 5.
CC -|- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS. TWO OF THE FIVE
CC CHAINS FORM A DIMER LINKED BY TWO INTERCHAIN DISULFIDE BONDS
CC LOCATED IN THE C-TERMINAL HEPTAPEPTIDE (SPECIFIC TO RAT CRP).
CC -|- PTM: THE LAST TWO CYSTEINES ARE INVOLVED EITHER IN INTERCHAIN
CC DISULFIDE BONDS OR IN AN INTRACHAIN BOND.
CC -|- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
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CC
CC EMBL; M83176; AAA0964.1; -
CC HSP; P02741; IGNH.
CC GlycoSuiteDB; P48199; -
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; pentaxin; 1.
CC PRINTS; PR00895; PENTAXIN.
CC SMART; SM00159; PTX; 1.
CC PROSITE; PS00289; PENTAXIN; 1.
KW Acute phase; Plasma; Calcium; Pentaxin; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 230 C-REACTIVE PROTEIN.
FT DOMAIN 20 230 PENTAXIN.
FT DISULFID 55 114
FT DISULFID 227 227 INTERCHAIN (BETWEEN MONOMERS A AND B).
FT DISULFID 228 228 INTERCHAIN (BETWEEN MONOMERS A AND B).
FT DISULFID 227 228 INTRACHAIN (IN MONOMERS C, D, AND E).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .).
FT SEQUENCE 230 AA; 25468 MW; D8CF6BFE72376309 CRC64;
SQ
Query Match 11.2%; Score 225.5; DB 1; Length 230;
Best Local Similarity 31.5%; Pred. No. 1.5e-10;
Matches 62; Conservative 32; Mismatches 90; Indels 13; Gaps 7;
QY 182 AILFPMRSKKIFGSHVPRMRLSESAICWIKATDVNLKTLFSGYTKRNPVEIQIYLS 241
DB 27 AFVPGVSATAYVSLAEASKKPLEAFTVCLYAHADVSRSFSTFSYATKTSFNEILLFWT 85
QY 242 Y-QSIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSGEGLTSLVNGELAAATVENVATGH 300
DB 86 RGQGFSTAVGPELLPSASIPVEP--THICATWESATGIVLWLDGK-PRVRKSLQKY 142
QY 301 IVEGGTILQTBKNGCGVGGDETLAFSGRLTGFTNWDVSLNSEEIRE--TGGAESCH 358
DB 143 IVGTNNAIILGQDQDS--YGGDFDQNSLVGDIGDVMWMDVLSPLSPQINAVVYGRVFS-- 198
QY 359 IRGNVGVGVTETQPHG 375
DB 199 --PVLNWRALKYETHG 213

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RESULT 12
PXNL_XENLA
ID PXNL_XENLA STANDARD; PRT; 416 AA.
AC P49263;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PENTRAXIN FUSION PROTEIN PRECURSOR.
GN PXNL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94052237; PubMed=7694301;
RA Seery L.T., Schoenberg D.R., Barbaux S., Sharp P.M., Whitehead A.S.;
RT "Identification of a novel member of the pentraxin family in Xenopus
RT laevis.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:263-270(1993).
CC -|- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
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CC
CC EMBL; L19881; AAC38013.1; -
CC HSP; P02743; ILGN.
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; pentaxin; 1.
CC PRINTS; PR00895; PENTAXIN.
CC SMART; SM00159; PTX; 1.
CC PROSITE; PS00289; PENTAXIN; 1.
KW Pentaxin; Signal.
FT SIGNAL 1 14 POTENTIAL.
FT CHAIN 15 416 PENTRAXIN FUSION PROTEIN.
FT DOMAIN 232 416 PENTAXIN.
FT DISULFID 251 311 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 416 AA; 47241 MW; 62EDE45E913A2BD7 CRC64;
SQ
Query Match 10.9%; Score 218.5; DB 1; Length 416;
Best Local Similarity 30.7%; Pred. No. 1.1e-09;
Matches 63; Conservative 28; Mismatches 69; Indels 45; Gaps 8;
QY 182 AILFPMRSKKIFGSHVPRMRLSESAICWIKATDVNLKTLFSGYTKRNPVEIQIYLS 230
DB 223 SPMFPKESINHVKLLPEKAMSLKAFKTLCKMKV---LLNVPENRETLFYSRTMEYDELN 278
QY 231 ---RNPYEIQLYSGSIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSGEGLTSLVNG 287
DB 279 LMIERDGRGLTWSGDGIIF-----PRMKFSEWNHPCUTWESKYGRTEFWLNG 327
QY 288 ELAATVEMATGHIYVEGGIQLQIGKEKNGCCVGGGDETLAFSGRLTGFTNWDVSLNSEE 347
DB 328 RRSATKV-YHQKNTVRSGGIVLLGQDQDS--YGGDFDQTSQFVGQIKDLKMKNKVLP 384
QY 348 I-----RETGAESCHIRGNVGV 366
DB 385 LKSLFKGREIG-----NGNIFDW 402
RESULT 13
CRP_MESAU

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ID * CRP_MESAU STANDARD: PRT: 225 AA.
AC P49262;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-REACTIVE PROTEIN PRECURSOR.
PTX1 OR CRP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91369977; PubMed=1892852;
RA Dowton S.B., Holden S.N.;
RT "C-reactive protein (CRP) of the Syrian hamster.";
RL Biochemistry 30:9531-9538(1991).
CC -!- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST
CC PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT
CC BINDING TO PHOSPHORYLCHOLINE (BY SIMILARITY).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- INDUCTION: BY INTERLEUKIN 1, INTERLEUKIN 6, AND TUMOR NECROSIS
CC FACTOR.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
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CC -----
DR EMBL; S56005; AAB19893.2; -
DR HSP; P02741; IGHN.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Acute phase; Plasma; Calcium; Pentaxin; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 225 C-REACTIVE PROTEIN.
FT DOMAIN 20 225 PENTAXIN.
FT DISULFID 55 116 BY SIMILARITY.
FT SEQUENCE 225 AA; 24822 MW; 00B439C45D58E05A CRC64;
Query Match 10.8%; Score 217.5; DB 1; Length 225;
Best Local Similarity 28.5%; Pred. No. 6e-10;
Matches 57; Conservative 38; Mismatches 92; Indels 13; Gaps 7;
QY 180 ETAILFPMSKIFGSHVPRMRLESFACIWW-KATDVLNKTILFSYGTGRNRYETQL 238
DB 25 KTAFFPKESANSYVSLAQAQSKTKLAKFTVCLHITELSTTRSFISYATKNSPNEILI 84
QY 239 YLSY-QSTVFVVGGENKLVAEMVSLGRWTHLCGTWNSEGLTSLVWNGELAAATTVEA 297
DB 85 FHSKDRGAFVGGGPEVLFKASEIEVP--THICASWESATGIAELWDGKPKVKI-LQ 141
QY 298 TGHIVPEGGIILQIQEKNGCCVGGFDETAFSGRLTGFNIWDSVLNNEEIRE--TGGAE 355
DB 142 KGYTVGTDAIILGQEQDS--YGGGFDAQNSLVGDIGVNMWDIVLSPEQINTVCVGGT- 198
QY 356 SCHIRGNVGVGTETIQPHG 375
DB 199 ---LDPSVLNMQALKYKVGQ 215
RESULT 14
```

```
FP_CRIMI STANDARD: PRT: 231 AA.
ID FP_CRIMI
AC P15697;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FEMALE PROTEIN PRECURSOR (FP) (SERUM AMYLOID P-COMPONENT).
OS Cricetulus migratorius (Armenian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10032;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90063074; PubMed=2479691;
RA Dowton S.B., Waggoner D.J.;
RT "Armenian hamster female protein (serum amyloid P component).
RT Comparison with the sex-regulated homolog in Syrian hamster.";
RL J. Immunol. 143:3776-3780(1989).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- MISCELLANEOUS: PLASMA CONCENTRATION OF FP ARE ALTERED BY SEX
CC STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.
CC -----
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CC -----
DR EMBL; M31610; AAA36981.1; -
DR PIR; A45814; A45814.
DR HSP; P07629; LHAS.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Pentaxin; Plasma; Acute phase; Calcium; Signal.
FT SIGNAL 1 19 FEMALE PROTEIN.
FT CHAIN 20 231 PENTAXIN.
FT DOMAIN 20 231 BY SIMILARITY.
FT DISULFID 55 114 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 231 AA; 26353 MW; A4D12A9DDE70B823 CRC64;
Query Match 10.6%; Score 212.5; DB 1; Length 231;
Best Local Similarity 28.7%; Pred. No. 1.5e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;
QY 184 LFPMSKIFGSHVPRMRLESFACIWW-KATDVLNKTILFSYGTGRNRYETQLY--- 239
DB 29 VPRESESDYVKILPRLEKPLENFILC-FRTYDLSRPHSLFSYNKNDNELLIKERM 87
QY 240 ----LSYQSIIVFVVGGENKLVAEMVSLGRWTHLCGTWNSEGLTSLVWNGELAAATTVE 295
DB 88 GEYGLYIENLGAIVRGVE-----EFASPVHFTCSWESSGIAEFVWG-IPWVKKG 137
QY 296 MATGHIVPEGGIILQIQEKNGCCVGGFDETAFSGRLTGFNIWDSVLNNEEIRETGGAE 355
DB 138 LKKGYTVKTPSTIILGQEQDN--YGGGFDSQSFVGMGMDLNMWDSVLTPEEKSV--YE 193
QY 356 SCHIRGNVGVGTETIQPHGGA 377
DB 194 GSWLEANILDWRTLNYEMSGYA 215
RESULT 15
CRP_MOUSE
```

ID CRP_MOUSE STANDARD; PRT; 225 AA.
AC P14847;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE C-REACTIVE PROTEIN PRECURSOR.
GN PTX1 OR CRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89050112; PubMed=3190681;
RA Ohnishi S., Maeda S., Nishiguchi S., Arao T., Shimada K.;
RT "Structure of the mouse C-reactive protein gene";
RL Biochem. Biophys. Res. Commun. 156:814-822(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA/J; TISSUE=Liver;
MEDLINE=90179719; PubMed=2310378;
RA Whitehead A.S., Zahedi K., Rits M., Mortensen R.F., Lelias J.M.;
RT "Mouse C-reactive protein: Generation of cDNA clones, structural
analysis, and induction of mRNA during inflammation.";
RL Biochem. J. 266:283-290(1990).
CC -!- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST
DEFENSE: IT PROMOTES AGGLUTINATION, BACTERIAL CAPSULAR SWELLING,
PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT
BINDING TO PHOSPHORYLCHOLINE.
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- INDUCTION: THE CONCENTRATION OF CRP IN PLASMA INCREASES GREATLY
DURING ACUTE PHASE RESPONSE TO TISSUE INJURY OR INFLAMMATION.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13588; CAA31928.1; -;
DR EMBL; X17496; CAA35531.1; -;
DR PIR; A31583; A31583.
DR PIR; S08286; S08286.
DR HSSP; P02741; 1GNH.
DR MGI; MGI:88512; Crp.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Acute phase; Plasma; Calcium; Pentaxin; Signal.
FT SIGNAL 1 19
FT CHAIN 20 225 C-REACTIVE PROTEIN.
FT DOMAIN 20 225 PENTAXIN.
FT DISULFID 55 116 BY SIMILARITY.
FT CONFLICT 134 134 A -> P (IN REF. 2).
SQ SEQUENCE 225 AA; 25361 MW; 155E6785E46043D9 CRC64;

Query Match 10.1%; Score 203.5; DB 1; Length 225;
Best Local Similarity 27.6%; Pred. No. 7.3e-09;
Matches 55; Conservative 39; Mismatches 90; Indels 15; Gaps 9;
QY 182 AILFPMRKKIFCSVHPVRPMLESFACI-WVKATDVLNKLTLFSYGTGRNPYEIQLYL 240
DB 27 AFVFPKSTSVSLAEAEKPLNFTVCLHFYTLSTVRSFVSFYATKKNSNDILIFW 86
QY 241 SY-QSIVFYVGGEEKNLVAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATG 299

Db 87 NKDKQVTFGVGAERFMVSEIPEAP--THICASWESATGIVEFWIDGK-AKVRKSLHKG 143
QY 300 HIV-PEGGILQIGOEKNGCCVGGFDETLAFSGRLTGFNWDVSLSNEETIRE--TGAES 356
Db 144 YTVGPDASII-LGQEQDS--YGGDFDAKQSLVGDIGDVMNMDVLSPEQINTVYVGGT-- 198
QY 357 CHIRGNIVGNGVTEIQPHG 375
Db 199 --LSPNVLNWRALNYKAQG 215

Search completed: December 18, 2001, 15:52:23
Job time: 182 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 31.68 Seconds
(without alignments)
1759.146 Million cell updates/sec

Title: US-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLTAILFCALWSAVLAENS.....NIVGWGVTETQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: . 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	14.7	429	11 070340	070340 mus musculus
2	293	14.6	494	11 035764	035764 rattus norv
3	289.5	14.4	432	11 P97738	P97738 rattus norv
4	280.5	14.0	202	5 Q98Y6	Q98Y6 tachyples
5	278	13.9	499	4 Q95502	Q95502 homo sapien
6	268.5	13.4	493	11 Q99J85	Q99J85 mus musculus
7	259.5	12.9	202	5 Q98Y8	Q98Y8 tachyples
8	259.5	12.9	202	5 Q98Y7	Q98Y7 tachyples
9	253.5	12.6	202	5 Q98Z4	Q98Z4 tachyples
10	249.5	12.4	202	5 Q98Z6	Q98Z6 tachyples
11	248.5	12.4	202	5 Q98Z9	Q98Z9 tachyples
12	247.5	12.3	202	5 Q9900	Q9900 tachyples
13	247.5	12.3	202	5 Q98Z8	Q98Z8 tachyples
14	246.5	12.3	202	5 Q98Z1	Q98Z1 tachyples
15	246.5	12.3	202	5 Q98Y9	Q98Y9 tachyples
16	245.5	12.2	202	5 Q98Z5	Q98Z5 tachyples
17	245.5	12.2	202	5 Q98Z0	Q98Z0 tachyples
18	242.5	12.1	202	5 Q98Z2	Q98Z2 tachyples
19	240.5	12.0	202	5 Q98Z7	Q98Z7 tachyples

20	229.5	11.4	3567	11 Q9ES77	Q9es77 mus musculu
21	228.5	11.4	202	5 Q98Y1	Q98y1 tachyples
22	228.5	11.4	202	5 Q98Y0	Q98y0 tachyples
23	225.5	11.2	240	11 Q9DIA3	Q9dia3 mus musculu
24	224.5	11.2	202	5 Q98X9	Q98x9 tachyples
25	219.5	10.9	202	5 Q98Z3	Q98z3 tachyples
26	219.5	10.9	202	5 Q98Y5	Q98y5 tachyples
27	213.5	10.6	202	5 Q98Y3	Q98y3 tachyples
28	212.5	10.6	202	5 Q98Y4	Q98y4 tachyples
29	211.5	10.5	223	11 Q63913	Q63913 cricetus
30	205.5	10.2	202	5 Q98Y2	Q98y2 tachyples
31	197.5	9.8	219	11 Q9D8J8	Q9d8j8 mus musculu
32	190	9.5	225	13 Q9PTT2	Q9ptt2 lepidobatra
33	187	9.3	222	6 Q15062	Q15062 sus scrofa
34	176	8.8	236	13 P79905	P79905 salmo salar
35	166.5	8.3	200	11 Q9D8V2	Q9d8v2 mus musculu
36	165	8.2	236	13 P79899	P79899 oncorhynch
37	155.5	7.7	224	6 Q19063	Q19063 sus scrofa
38	138	6.9	606	2 Q86584	Q86584 streptomyce
39	135.5	6.8	558	5 Q76933	Q76933 drosophila
40	135.5	6.8	558	5 Q9V3N9	Q9v3n9 drosophila
41	119.5	6.0	1627	4 Q13219	Q13219 homo sapien
42	117	5.8	1503	2 Q52973	Q52973 bacillus ci
43	115	5.7	4199	2 P74440	P74440 synecocyst
44	114	5.7	521	4 Q9Y5J1	Q9y5j1 homo sapien
45	112	5.6	1000	5 Q9NKG8	Q9nkg8 leishmania

ALIGNMENTS

RESULT 1
ID 070340 PRELIMINARY; PRT; 429 AA.
AC 070340;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE NEURONAL PENTRAXIN 2.
GN NPTX2 OR NP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Perin M.S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Perin M.S.;
RT "Mouse neuronal pentraxin 2 gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049124; AAC05131.1; -;
DR EMBL; AF318618; AAK06745.1; -;
DR HSSP; P06205; LLIM.
DR MGD; MGI:1858209; Nptx2.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
SQ SEQUENCE . 429 AA; 47136 MW; 638EED14C4CECA28 CRC64;

Query Match 14.7%; Score 295; DB 11; Length 429;

Best Local Similarity 25.5%; Pred. No. 4.1e-15;

Matches 98; Conservative 56; Mismatches 122; Indels 108; Gaps 14;

QY 67 QMRERMLLQATDDVLRLGELQRLRELGRLLA--ESLA-----RPGCAPGAPAE 110

DB 66 QLRETVVQQ--KETLGAQREAIKRLTGKLRCEGLAGGKARGTKMGDLPRDPGHVVE 123

```
QY 111 -----ARLTSALDELLO-----ATRDAGRRLARME----- 135
DB 124 QLSRLQTLKDLRLSLELQTLNVSAGLPSDFEVLQRLGELEROLLKRAELEDK 183
QY 136 -----GAERORPEAGRAALAELELQTRADLHAGVQWAARSWLPAGCETAILFPMS 189
DB 184 LLHNETSARHOKTESTNALQLLQRTLELERNISAFKSPDAF-----KVSLPLRT 231
QY 190 KKFSGVHPVRPMRLESFSAIWKAT-----DVLNKTILFSYGTGRNRYE 235
DB 232 NYLFGKIKKTLPL-ELYAFTICLWRSSASPGIGTFFSYAVPGQANEIVLIENG--NNPIE 288
QY 236 IQLYLSYQSIYFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSBEGTLSTLWNGELAATT 293
DB 289 LLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGMWEAFQDGEKLG 333
QY 294 VEMATCHIVPEGGLIQGKNGCCVGGGDETLAFSGRLTGNINWDSVLSNEIRETGG 353
DB 334 ENLAPWHPKIPGGVILILGQEQD--TVGGRFDATQAFVGEISQFNINWDRVLRQAQEI 391
QY 354 AESCHIRGNIVGWGVTIOPHGA 377
DB 392 C-STNMPGNIIPWVDNVDVEGGA 414

RESULT 2
ID 035764 PRELIMINARY; PRT; 494 AA.
AC 035764;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RA Dadds D.C., Omeis I.A., Cushman S.J., Helms J.A., Perin M.S.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005099; AAB62885.1;
DR HSSP: P02743; ISAC.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin; 1.
DR PRINTS: PR00895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
R SEQUENCE 494 AA; 52370 MW; FEC996CA311E40E2 CRC64;
Q

Query Match 14.6%; Score 293; DB 11; Length 494;
Best Local Similarity 28.2%; Pred. No. 7.1e-15;
Matches 98; Conservative 58; Mismatches 123; Indels 68; Gaps 17;

QY 56 WDK--LFLIMLNSQMRMLQATDDVLRLGELRLREEL---CRLAESLRPCAPGAPAE 110
DB 179 WSPALLVELENVR-----ALDRIERIEQELPARGNLSSAPAPAVPTA--- 224
QY 111 ARLTSALDELLOATRDAGRRLARMEAGRAALAELELQTRADLHAGVQW 169
DB 225 --LHKNDEL-----EGQLAKVLALEKER-----AALSHGSHQORQEVEKELDALQGR 271
QY 170 AARSWLPAGCET-----AILEPMRSKKIFGSHVHPVRPMRLESFSAIWKATDVLNKT 222
DB 272 VAE--LEHGSSAYSPDPAFKVSIPIRNMYARVRAVP-ELYAFTACMWLRSR----- 322
QY 223 ILFSYGT-KRNPEYIQLYLSYQSIYFVVGGE-----NKLVAEMVSL--GRWTHLCGT 273
DB 323 ---SGSGGOTPFPSYVPGQANEIVLIENGAGLEPMELLINDKVAQLPLSKDSNWHHCIA 379
QY 354 AESCHIRGNIVGWGVTIOPHGA 377
DB 392 C-STNMPGNIIPWVDNVDVEGGA 414
```

```
DB 380 WTRDGLWSAYQDELGRSGENLAAWHPKIPGHGILILGQEQD--TLGGRFDATQAFVGD 437
QY 334 TGNINWDSVLSNEIRETGAESC--HIRGNIVGWGVTIOPHGAQ 378
DB 438 AQNLNDHALTPAQLV---GIANTCTGPMGNVLPWEDKLVFAFGAK 481

RESULT 3
ID P97738 PRELIMINARY; PRT; 432 AA.
AC P97738;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=96256683; PubMed=8786423;
RA Tsui C.C., Copeland N.G., Gilbert D.J., Jenkins N.A., Barnes C.,
RA Worley P.F.;
RT "Narp, a novel member of the pentraxin family, promotes neurite
RT outgrowth and is dynamically regulated by neuronal activity.";
RL J. Neurosci. 16:2463-2478(1996).
DR EMBL: S82649; AAB46783.1;
DR HSSP: P06205; ILIM.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin; 1.
DR PRINTS: PR00895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTAXIN; 1.
R SEQUENCE 432 AA; 47429 MW; DD642A6AA323D24A CRC64;
Q

Query Match 14.4%; Score 289.5; DB 11; Length 432;
Best Local Similarity 27.4%; Pred. No. 1.1e-14;
Matches 90; Conservative 51; Mismatches 118; Indels 69; Gaps 12;

QY 81 LRGELORLREELGRLAESLRPCAPGAPAEARLTSALDELLO-----ATRDAGRRLARME 135
DB 128 LRSRLQTLKDLRLSLELQTLNVSAGLPSDFEVLQRLGELEROLLKRAELEDK 182
QY 136 -----GAERORPEAGRAALAELELQTRADLHAGVQWAARSWLPAGCETAILF 185
DB 183 DEKSLHNETSARHOKTESTNALQLLQRTLELERNISAFKSPDAF-----KVSL 230
QY 186 PMRSKKIFGSHVHPVRPMRLESFSAIWKAT-----DVLNKTILFSYGTGR 231
DB 231 PLRTNLYGKIKKTLPL-ELYAFTICLWRSSASPGIGTFFSYAVPGQANEIVLIENG--N 287
QY 232 NPYEIQLYLSYQSIYFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSBEGTLSTLWNGEL 289
DB 288 NPTELLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGMWEAFQDGEK 332
QY 290 AATVTVMATCHIVPEGGLIQGKNGCCVGGGDETLAFSGRLTGNINWDSVLSNEEIR 349
DB 333 LGTGENLAPWHPKIPGGVILILGQEQD--TVGGRFDATQAFVGEISQFNINWDRVLRQAQEI 390
QY 350 ETGGAESCHIRGNIVGWGVTIOPHGA 377
DB 391 NIANC-STNMPGNIIPWVDNVDVEGGA 417

RESULT 4
ID Q98Y6 PRELIMINARY; PRT; 202 AA.
AC Q98Y6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 21.12 Seconds
(without alignments)
1374.172 Million cell updates/sec

Title: us-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLAIFCALWSAVLAENS.....NIVGWTVEIQPHGAQYVS 381

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: -219241 seqs, 76174552 residues

i number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2007	100.0	381	2 A44323	pentaxin PTX3 prec
2	296.5	14.8	427	2 A55496	apexin precursor -
3	289.5	14.4	432	2 T10894	neuronal pentraxin
4	256.5	12.8	242	2 A25192	C-reactive protein
5	253.5	12.6	218	2 C25193	C-reactive protein
6	252.5	12.6	218	2 B25193	C-reactive protein
7	249.5	12.4	242	2 B25192	C-reactive protein
8	248.5	12.4	242	2 C25192	C-reactive protein
9	225.5	11.2	230	2 A42579	C-reactive protein
10	217.5	10.9	225	2 A40326	C-reactive protein
11	212.5	10.6	231	2 A45814	female protein pre
12	211.5	10.5	223	2 I59479	serum amyloid P -
13	203.5	10.1	225	2 A31563	C-reactive protein
14	200.5	10.0	225	2 C1JB	C-reactive protein
15	192.5	9.6	211	2 A4177	female protein - g
16	192.5	9.6	225	2 JX0259	C-reactive protein
17	187.5	9.3	234	2 A48593	serum amyloid p-co
18	184.5	9.2	224	1 CJHU	C-reactive protein
19	183.5	9.1	228	2 S11473	serum amyloid P-co
20	181	9.0	238	2 A45487	C-reactive protein
21	165	8.2	224	2 A30528	serum amyloid P-co
22	164.5	8.2	223	2 JX0260	serum amyloid P-co
23	161.5	8.0	223	1 YLHUP	serum amyloid p-co
24	138	6.9	606	2 T37217	probable ATP/GTP b
25	119.5	6.0	1627	2 S65464	pregnancy-associat
26	117	5.8	1503	2 T18266	cycloinulo-oligosa
27	115	5.7	4199	2 S76412	hypothetical prote
28	112.5	5.6	899	2 S12319	pre-mRNA splicing
29	110	5.5	472	2 G83335	outer membrane pro

30 106 5.3 320 2 T08493 probable regulator
31 106 5.3 472 2 T30831 hypothetical prote
32 99 4.9 304 2 JX0209 lectin, galactose/
33 98.5 4.9 2101 2 A42184 nuclear mitotic ap
34 97.5 4.9 856 2 E75292 GDEF family prote
35 97 4.8 775 2 B82671 general secretory
36 97 4.8 1170 2 A57650 repair protein XPG
37 96.5 4.8 774 2 D83208 probable ferredoxi
38 95.5 4.8 316 2 JC6549 apolipoprotein E p
39 95.5 4.8 3972 2 S75251 hypothetical prote
40 95 4.7 284 2 A33085 hypothetical prote
41 95 4.7 3063 2 S55505 tropomyosin - bloo
42 95 4.7 10223 2 T30225 fatty-acid synthas
43 94 4.7 527 1 S25478 polyketide synthas
44 92 4.6 306 2 A42230 heat shock transcr
45 92 4.6 400 2 T46526 lectin M-ASGP-BP p
probable hydroxyyla

ALIGNMENTS

RESULT 1

A44323
pentaxin PTX3 precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C:Accession: A44323; S18947; S17069; S37597
R:Breviarlo, F.; d'Aniello, E.M.; Golay, J.; Peri, G.; Bottazzi, B.; Bairoch, A.; Sac
J. Biol. Chem. 267, 22190-22197, 1992
A:Title: Interleukin-1-inducible genes in endothelial cells. Cloning of a new gene re
A:Reference number: A44323; MUID:93054498
A:Accession: A44323
A:Molecule type: mRNA
A:Residues: 1-47, 'A', 49-381 <BR1>
A:Experimental source: umbilical vein endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIP:117003)
R:Breviarlo, F.; d'Aniello, E.M.; Golay, J.; Bairoch, A.; Dejana, E.; Mantovani, A.;
submitted to the EMBL Data Library, January 1992
A:Description: Cloning of a new member of the pentaxin gene family from interleukin-1
A:Reference number: S18947
A:Accession: S18947
A:Molecule type: mRNA
A:Residues: 1-381 <BR2>
A:Cross-references: EMBL:X63613; NID:g35796; PIDN:CAA45158.1; PID:g35797
C:Genetics:
A:Gene: GDB:PTX3
A:Cross-references: GDB:136459
A:Map position: 3q25-3q25
F:1-17/Domain: signal sequence #status predicted <SIG>

Query Match 100.0%; Score 2007; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.8e-151;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHLAIFCALWSAVLAENSDDYDLMYVNLNDNEINDGLHPTEDPTPCDCGSEHSDKLF 60
Db 1 MHLAIFCALWSAVLAENSDDYDLMYVNLNDNEINDGLHPTEDPTPCDCGSEHSDKLF 60
Qy 61 IMLENSOMRRLQATDDVLRGELQRLREELGRLAESLARPCAPAPAEARLTSSALDEL 120
Db 61 IMLENSOMRRLQATDDVLRGELQRLREELGRLAESLARPCAPAPAEARLTSSALDEL 120
Qy 121 LQATRDAGRRLARMEGAQORPEAGRALAAVLEELROTRADLHAVQGWAAARSLPACGE 180
Db 121 LQATRDAGRRLARMEGAQORPEAGRALAAVLEELROTRADLHAVQGWAAARSLPACGE 180
Qy 181 TAILFPNRSKKIFGSHVHVRPMRLSFACIWKATDVLNKTILFSYCTKRNPIQLYL 240
Db 181 TAILFPNRSKKIFGSHVHVRPMRLSFACIWKATDVLNKTILFSYCTKRNPIQLYL 240
Qy 241 SYQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSBGLTSLWVNGELAATTVMATGH 300
Db 241 SYQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSBGLTSLWVNGELAATTVMATGH 300

Db 241 STQSTIVFVVGGENKLVAFAMVSLGRWTHLCGTWNSERGLTSLVWNGELAAATVEMATCH 300
QY 301 IVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFTNWDVSLNSEEIRGTGAESCHIR 360
Db 301 IVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFTNWDVSLNSEEIRGTGAESCHIR 360
QY 361 GNIWGVGVTETQPHGGAQYVS 381
Db 361 GNIWGVGVTETQPHGGAQYVS 381
RESULT 2
A55496
apexin precursor - guinea pig
N:Alternate names: 50K pentaxin, acrosomal
C:Species: Cavia porcellus (guinea pig)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55496; A55497
R:Noland, T.D.; Friday, B.B.; Maulit, M.T.; Gerton, G.L.
J. Biol. Chem. 269, 32607-32614, 1994
Title: The sperm acrosomal matrix contains a novel member of the pentaxin family of ca
Reference number: A55496; MUID:95096119
A:Accession: A55496
A:Molecule type: mRNA
A:Residues: 1-427 <NOL>
A:Cross-references: GB:U13234; NID:g595676; PIDN:AAA64994.1; PID:g595677
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Reid, M.S.; Blobel, C.P.
J. Biol. Chem. 269, 32615-32620, 1994
A:Title: Apexin, an acrosomal pentaxin.
A:Reference number: A55497; MUID:95096120
A:Accession: A55497
A:Molecule type: mRNA
A:Residues: 1-139,142-427 <REI>
A:Cross-references: GB:U13236; NID:g595678; PIDN:AAA64995.1; PID:g595679
A:Note: parts of this sequence were confirmed by peptide sequencing
C:Keywords: glycoprotein; sperm
F:148,185,389/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.8%; Score 296.5; DB 2: Length 427;
Best Local Similarity 24.5%; Pred. No. 9.2e-16;
Matches 94; Conservative 60; Mismatches 121; Indels 109; Gaps 14;
QY 67 QMRERMLQ-----ATDDVLRGELQRLREELG-----RLAESLA 100
Db 65 QURETVWQKETLGAQREARELTSKLARCEGLMAGKAESSKDTMGDLPRDPSRVVEOLS 124
101 RPCA-----PCAPAEAR--LTSALDELLOQTRDAGRRLARME---- 135
Db 125 RSLQVLKDRLESLEQLRTNASNTGLPSDFREVLQRLGEL---ERQLLRKVAELEDKES 181
QY 136 -----GAEQRPPEAGRALAAVLEELQTRADLHAGVGAARSLPAGCETAILFPMS 189
Db 182 LHNETSAAHQKTENTLNAQLQRTVTELRGNSAFKSPDAF-----KVSLEPRT 229
QY 190 KKFQSVHPVRPMRLSEFSACIWKAT-----DVLNKTILFSYGTGRNPE 235
Db 230 NYLYGKIKKTLF-ELYFTICLWLRSASPGIGTFPSVAVPQANEIVLIEMG--NNPIE 286
QY 236 IQLYLSYSQSVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSERGLTSLVWNGELAATT 293
Db 287 LLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGLWEAFQDGEKLTG 331
QY 294 VEMATGHIVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFTNWDVSLNSEEIRGTGG 353
Db 332 ENLAPWHPIKSGVLLIQEQD--TVGGRFDATQAFVGLSOFNIDRWDRVLRPQELSNIAN 389
QY 354 AESCHIRGNIVGWGVTETQPHGGA 377
Db 390 C-SLNAGNIIPWVDNNVDVFGGA 412

RESULT 3
TI0894
neuronal pentraxin - rat
C:Species: Rattus sp. (rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: TI0894
R:Tsui, C.C.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barnes, C.; Worley, P.F.
J. Neurosci. 16, 2463-2478, 1996
A:Title: Narp, a novel member of the pentraxin family, promotes neurite outgrowth and
A:Reference number: 217203; MUID:96256683
A:Accession: TI0894
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <TSU>
A:Cross-references: EMBL:S82649; NID:g1835928; PIDN:AA846783.1; PID:g1835929
C:Genetics:
A:Gene: Narp
C:Function:
C:Keywords: pentraxin
Query Match 14.4%; Score 289.5; DB 2: Length 432;
Best Local Similarity 27.4%; Pred. No. 3.3e-15;
Matches 90; Conservative 51; Mismatches 118; Indels 69; Gaps 12;
QY 81 LRGELOLRREELGRLAESLARCPAGPAEARLTSAIDELLO-----ATRDAGRRLARME 135
Db 128 LRSRLQTLKDL-----ESLEQLQHTNA-SNAGLPDFREVLQRLGELERQLLRKVAELE 182
QY 136 -----GAEQRPPEAGRALAAVLEELQTRADLHAGVGAARSLPAGCETAILF 185
Db 183 DEKSLHNETSAAHQKTENTLNAQLQRTVTELRGNSAFKSPDAF--DVLNKTILFSYGTGR 231
QY 186 PMSKKIKGSHVHPVRPMRLSEFSACIWKAT-----DVLNKTILFSYGTGR 231
Db 231 PLRTNYLYGKIKKTLF-ELYFTICLWLRSASPGIGTFPSVAVPQANEIVLIEMG--N 287
QY 232 NPYEIQLYLSYSQSVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSERGLTSLVWNGEL 289
Db 288 NPIELLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGLWEAFQDGEK 332
QY 290 AATVEMATGHIVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFTNWDVSLNSEEIR 349
Db 333 LGTGENLAPWHPIKSGVLLIQEQD--TVGGRFDATQAFVGLSOFNIDRWDRVLRQAETI 390
QY 350 ETGGAESCHIRGNIVGWGVTETQPHGGA 377
Db 391 NIANC-STNMPGNIIIPWVDNNVDVFGGA 417
RESULT 4
A25192
C-reactive protein chain 1.4 precursor - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 30-Jun-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C:Accession: A25192; A25193
R:Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A:Title: Isolation and characterization of Limulus C-reactive protein genes.
A:Reference number: A25551; MUID:86278105
A:Accession: A25192
A:Molecule type: DNA
A:Residues: 1-242 <NGU>
A:Cross-references: GB:M14024; NID:g156631; PIDN:AAA28268.1; PID:g156632
A:Note: the authors translated the codon ACC for residue 31 as Val
R:Nguyen, N.Y.; Suzuki, A.; Boykins, R.A.; Liu, T.Y.
J. Biol. Chem. 261, 10456-10465, 1986
A:Title: The amino acid sequence of Limulus C-reactive protein. Evidence of polymorph
A:Reference number: A25193; MUID:86278106
A:Accession: A25193
A:Molecule type: DNA
A:Residues: 25-242 <NG2>

RESULT 8
C25192
C-reactive protein chain 1.1 precursor - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 20-Aug-1999

C:Accession: C25192
R.Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A:Title: Isolation and characterization of Limulus C-reactive protein genes.
A:Reference number: A92551; MUID:86278105
A:Accession: C25192
A:Molecule type: DNA
A:Residues: 1-242 <NGU>
A:Cross-references: GB:M14026; NID:gl56635; PIDN:AAA28270.1; PID:gl56636
C:Genetics:
A:Start codon: ATG.
C:Superfamily: C-reactive protein

Query Match 12.4%; Score 248.5; DB 2; Length 242;
Best Local Similarity 28.4%; Pred. No. 2.7e-12;
Matches 57; Conservative 44; Mismatches 91; Indels 9; Gaps 5;
QY 183 ILPPMRSKKIFGSHVPRPM-RLEFSACIWKATDVLNKTILFSYGTGRNPNVEIOLYLS 241
34 VKFPSSSPFPLVWVGTLPLDLEITLCYWFKNRLKGLHMFYATAKKONELLTLD 93
QY 242 YQS--IVFVVGGENKLVAMVSLGRWTHLCGTWNSSEGLTSLWNG-ELAATTVMAT 298
DB 94 EOGDFLNFVHGAQLKVCQPNKTHIGKWHVCHTWSSEGEATIAVDGFHCKGNATGIAV 153
QY 299 GHIVPEGGILQIGKRGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR---ETGGAE 355
DB 154 GRTLSGGVLVLCQDQDS--VGGKFDATQSGELSELNWNVLNHEQIKYLSKCAHPS 211
QY 356 SCHIRGNIVGWVTEIQPHG 376
DB 212 ERHYGNIIQWDKTFKAYDG 232

RESULT 9
A42579
C-reactive protein precursor - rat
N:Alternate names: CRP
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: A42579
R:Rassouli, M.; Sambasivam, H.; Azadi, P.; Dell, A.; Morris, H.R.; Nagpurkar, A.; Mooker
J. Biol. Chem. 267, 2947-2954, 1992
A:Title: Derivation of the amino acid sequence of rat C-reactive protein from cDNA clones
A:Reference number: A42579; MUID:92147634
A:Accession: A42579
Molecule type: mRNA
Residues: 1-230 <RAS>
A:Cross-references: GB:M83176; NID:G203591; PIDN:AAA40964.1; PID:G203592
A:Note: sequence extracted from NCBI backbone (NCBIP:80758)
C:Superfamily: C-reactive protein
C:Keywords: acute phase; liver; pentamer; pentraxin; plasma

Query Match 11.2%; Score 225.5; DB 2; Length 230;
Best Local Similarity 31.5%; Pred. No. 1.6e-10;
Matches 62; Conservative 32; Mismatches 90; Indels 13; Gaps 7;
QY 182 AILPPMRSKKIFGSHVPRPMRLESFACIWKATDVLNKTILFSYGTGRNPNVEIOLYLS 241
DB 27 AFVPGVSATAYVSLAESKKEAFVCLYAH-AVRSFISFATKTSFNEILLFWT 85
QY 242 Y-QSIVFVVGGENKLVAMVSLGRWTHLCGTWNSSEGLTSLWNGELAATTVMATGH 300
DB 86 RGQGFSTAVGPELFSASIEPEV--THICATWESATGIVELWLDGK-PRVRKSLQGY 142
QY 301 IVPEGGILQIGKRGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR--TGGAE 358
DB 143 IVGTNASIILGQEQDS--YGGGFDANGSLVDIGDVMNMDIVLSPEQINTVCVGGT-- 198
QY 359 IRGNIVGWVTEIQPHG 375

DB 199 --PNVLNWRALKVETHG 213

RESULT 10
A40326
C-reactive protein precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
C:Accession: A40326; B40326
R:Dowton, S.B.; Hoiden, S.N.
Biochemistry 30, 9531-9538, 1991
A:Title: C-reactive protein (CRP) of the Syrian hamster.
A:Reference number: A40326; MUID:91369977
A:Accession: A40326
A:Molecule type: DNA
A:Residues: 1-225 <DOW>
A:Cross-references: GB:J05343; GB:S56005
A:Note: the authors translated the codon CTA for residue 199 as Asp and GAC for resid
A:Accession: B40326
A:Molecule type: mRNA
A:Residues: 1-225 <DOW2>
A:Cross-references: GB:J05343; GB:S56005
C:Comment: This protein, unlike its homolog SAP (serum amyloid P component), is not g
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein
C:Keywords: pentamer
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-225/Product: C-reactive protein #status predicted <MAT>

Query Match 10.8%; Score 217.5; DB 2; Length 225;
Best Local Similarity 28.5%; Pred. No. 6.8e-10;
Matches 57; Conservative 38; Mismatches 92; Indels 13; Gaps 7;

QY 180 ETAILPPMRSKKIFGSHVPRPMRLESFACIWK-RATDVLNKTILFSYGTGRNPNVEIOL 238
DB 25 KTAFFVPKESANSYVSLAQSKKTLKAFVCLHIFTTELSTTRSFISYATKNSPNEILI 84
QY 239 YLSY-OSIVFVVGGENKLVAMVSLGRWTHLCGTWNSSEGLTSLWNGELAATTVEMA 297
DB 85 FWSKDRGYAFVGGPEVLFKASIEPEV--THICASWESATGIAELWVDGKPKVKRI-LQ 141
QY 298 TGHIVPEGGILQIGKRGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR--TGGAE 355
DB 142 KGYTVGTDAISILGQEQDS--YGGGFDANGSLVDIGDVMNMDIVLSPEQINTVCVGGT- 198
QY 356 SCHIRGNIVGWVTEIQPHG 375
DB 199 ---LDFSVLNWQALKYKVGQ 215

RESULT 11
A45814
female protein precursor - Armenian hamster
C:Species: Cricetus migratorius (Armenian hamster)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: A45814
R:Dowton, S.B.; Waggoner, D.J.
J. Immunol. 143, 3776-3780, 1989
A:Title: Armenian hamster female protein (serum amyloid P component). Comparison with
A:Reference number: A45814; MUID:90063074
A:Accession: A45814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <DOW>
A:Cross-references: GB:M31610; NID:gl91075; PIDN:AAA36981.1; PID:g304506
C:Superfamily: C-reactive protein

Query Match 10.6%; Score 212.5; DB 2; Length 231;
Best Local Similarity 28.7%; Pred. No. 1.8e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;

Qy 184 LFMRSKKIFGSHVPRMRLSFSAIWKATDVNLKTLFSGYTKRNPYEIOLY----- 239
Db 29 VFPRESSESDYVKLPRLKPLENFTLC-FRTYTDLSRPHSLFSYNTKNDKNELLIYKERM 87
Qy 240 ----LSYQSVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLTSLVWNGELAATVE 295
Db 88 GEYGLYIENGAIVRGVE-----EFASPVHFCTSWESSGIAEFWNG-IPWVKKG 137
Qy 296 MATGHIVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRETGGAE 355
Db 138 LKKGTYVTQPSIILGQODN--YGGGFDKQSQFVGEMGLNMDSVLTPEIKSV--YE 193
Qy 356 SCHIRGNIVGNGVTEIQPHGGA 377
Db 194 GSWLEANILDRWTLNLYEMSGYA 215

RESULT 12

Qy 9479
Species: Cricetus migratorius (Armenian hamster)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I59479
R:Rudnick, C.M.; Dowton, S.B.
Scand. J. Immunol. 38, 445-450, 1993
A:Title: Serum amyloid-P component of the Armenian hamster: gene structure and comparison
A:Reference number: I59479; MUID:94053543
A:Accession: I59479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-223 <RES>
A:Cross-references: GB:567057; NID:g452889; PIDN:AAB28726.1; PID:g452890
C:Genetics:
A:Gene: SAP
A:Introns: 22/1
C:Superfamily: C-reactive protein

Query Match 10.5%; Score 211.5; DB 2; Length 223;
Best Local Similarity 28.7%; Pred. No. 2e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;
Qy 184 LFMRSKKIFGSHVPRMRLSFSAIWKATDVNLKTLFSGYTKRNPYEIOLY----- 239
Db 29 VFPRESSESDYVKLPRLKPLENFTLC-FRTYTDLSRPHSLFSYNTKNDKNELLIYKERM 87
Qy 240 ----LSYQSVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLTSLVWNGELAATVE 295
Db 88 GEYGLYIENGAIVRGVE-----EFASPVHFCTSWESSGIAEFWNG-IPWVKKG 137
Qy 296 MATGHIVPEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRETGGAE 355
Db 138 LKKGTYVTQPSIILGQODN--YGGGFDKQSQFVGEMGLNMDSVLTPEIKSV--YE 193
Qy 356 SCHIRGNIVGNGVTEIQPHGGA 377
Db 194 GSWLEANILDRWTLNLYEMSGYA 215

RESULT 13

A:Accession: A31583
C-reactive protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C:Accession: A31583; S08286
R:Ohnishi, S.; Maeda, S.; Nishiguchi, S.; Arao, T.; Shimada, K.
Biochem. Biophys. Res. Commun. 156, 814-822, 1988
A:Title: Structure of the mouse C-reactive protein gene.
A:Reference number: A31583; MUID:89050112
A:Accession: A31583
A:Molecule type: DNA
A:Residues: 1-225 <OHN>

A:Cross-references: GB:X13588; NID:g50571; PIDN:CAA31928.1; PID:g295904
R:Whitehead, A.S.; Zahedi, K.; Rits, M.; Mortensen, R.F.; Lellias, J.M.
Biochem. J. 266, 283-290, 1990
A:Title: Mouse C-reactive protein. Generation of cDNA clones, structural analysis, and
A:Reference number: S08286; MUID:90179719
A:Accession: S08286
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133, 'P', 135-225 <WHI>
A:Cross-references: EMBL:X17496; NID:g50563; PIDN:CAA35531.1; PID:g50564
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein

Query Match 10.1%; Score 203.5; DB 2; Length 225;
Best Local Similarity 27.6%; Pred. No. 8.7e-09;
Matches 55; Conservative 39; Mismatches 90; Indels 15; Gaps 9;
Qy 182 AILFPMRSKKIFGSHVPRMRLSFSAIWKATDVNLKTLFSGYTKRNPYEIOLYL 240
Db 27 AFVFPKESDTSYVSLAEASKKPLNTFTVCLHFTALSTVRSFVSFYATKKNSNDILIFW 86
Qy 241 SY-QSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLTSLVWNGELAATVEMATG 299
Db 87 NDKQYTFEGVGAERFVWSEIPEAP--THICASWESATGIVEFWIDCK-AKVRKSLHKG 143
Qy 300 HIV-PEGIILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRE--TGGAES 356
Db 144 YTVGPDSII-LGQODS--YGGDFDAKQSLVDIGDYNMDFVLSPEQINTVYVGGT-- 198
Qy 357 CHIRGNIVGNGVTEIQPHG 375
Db 199 --LSPNVLNWRALNYKAQG 215

RESULT 14

CJRB
C-reactive protein precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 05-Apr-1983 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C:Accession: A25605; A25583; A03202
R:Syn, C.; Gotschlich, E.C.; Liu, T.Y.
J. Biol. Chem. 261, 5473-5479, 1986
A:Title: Rabbit C-reactive protein. Biosynthesis and characterization of cDNA clones.
A:Reference number: A25605; MUID:86168292
A:Accession: A25605
A:Molecule type: mRNA
A:Residues: 1-225 <SVI>
A:Cross-references: GB:M13497; NID:g164901; PIDN:AAA31206.1; PID:g164902
R:Hu, S.I.; Miller, S.M.; Samols, D.
Biochemistry 25, 7834-7839, 1986
A:Title: Cloning and characterization of the gene for rabbit C-reactive protein.
A:Reference number: A25583; MUID:87101075
A:Accession: A25583
A:Molecule type: DNA
A:Residues: 1-9, 'T', 11-107, 'I', 109-192, 'I', 194-225 <HUS>
A:Cross-references: GB:M14538; NID:g164899; PIDN:AAA75403.1; PID:g164900
R:Wang, C.M.; Nguyen, N.Y.; Yonaha, K.; Robey, F.; Liu, T.Y.
J. Biol. Chem. 257, 13610-13615, 1982
A:Title: Primary structure of rabbit C-reactive protein.
A:Reference number: A03202; MUID:83058861
A:Accession: A03202
A:Molecule type: protein
A:Residues: 21-45, 'T', 47-49, 'L', 51-83, 'F', 85, 105, 'KE', 108, 'I', 110, 'Y', 112-166, 'W', 168
A:Note: 62-Lys and 108-Asp were also found
A:Note: Asp-61, Arg-76, Arg-77, and Glu-81 may be involved in the calcium-dependent b
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein
C:Keywords: acute phase; pentamer; plasma
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-225/Product: C-reactive protein #status experimental <MAT>

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OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:20 ; Search time 18.72 Seconds
(without alignments)
458.000 Million cell updates/sec

Title: US-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLALFALMSAVLAENS.....NIVGNGVTETIQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

1 number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	39.3	178	1	US-07-929-580B-2
2	294	14.6	430	1	US-08-631-607-7
3	289.5	14.4	432	1	US-08-631-607-2
4	277	13.8	426	1	US-08-631-607-6
5	269.5	13.4	232	1	US-08-631-607-5
6	225.5	11.2	211	1	US-08-631-607-4
7	184.5	9.2	201	1	US-07-929-580B-3
8	184.5	9.2	225	1	US-07-708-885B-1
9	184.5	9.2	225	1	US-07-714-386-1
10	184.5	9.2	225	1	US-07-708-888A-1
11	183.5	9.1	208	1	US-08-631-607-3
12	160.5	8.0	201	1	US-07-929-580B-5
13	146.5	7.3	223	1	US-07-708-885B-3
14	146.5	7.3	223	1	US-07-714-386-3
15	146.5	7.3	223	1	US-07-708-888A-3
16	98.5	4.9	2101	1	US-08-466-390-4
17	98.5	4.9	2101	1	US-08-470-350-4
18	98.5	4.9	2101	1	US-08-467-781-4
19	98.5	4.9	2101	1	US-08-195-487-4
20	98.5	4.9	2101	2	US-08-483-924-4
21	98.5	4.9	2101	4	US-09-452-294-1
22	98.5	4.9	2101	5	PCT-US93-06160-4
23	98	4.9	2293	4	US-09-368-590-2
24	95.5	4.8	2627	2	US-08-751-189-3
25	95.5	4.8	2627	2	US-09-060-836-3
26	95.5	4.8	2627	4	US-09-184-445-3
27	91.5	4.6	280	1	US-08-781-562-4

28 91.5 4.6 566 2 US-08-533-669A-8 Sequence 8, Appl1
29 91.5 4.6 566 2 US-08-511-872-2 Sequence 2, Appl1
30 90.5 4.5 4545 2 US-08-804-227C-14 Sequence 14, Appl1
31 90.5 4.5 4550 2 US-08-804-227C-8 Sequence 8, Appl1
32 90.5 4.5 4550 2 US-08-804-198-2 Sequence 2, Appl1
33 88 4.4 502 4 US-09-413-814-106 Sequence 106, App
34 88 4.4 2860 2 US-08-826-267-2 Sequence 2, Appl1
35 87.5 4.4 3491 2 US-07-642-734C-2 Sequence 2, Appl1
36 87.5 4.4 3491 3 US-08-439-009A-2 Sequence 2, Appl1
37 87 4.3 897 1 US-08-095-737-4 Sequence 4, Appl1
38 87 4.3 897 1 US-08-480-145-4 Sequence 4, Appl1
39 87 4.3 897 2 US-08-477-389-4 Sequence 2, Appl1
40 86 4.3 594 2 US-08-910-856-2 Sequence 2, Appl1
41 86 4.3 5087 4 US-09-144-085-1 Sequence 1, Appl1
42 84.5 4.2 341 1 US-08-190-802A-45 Sequence 45, Appl1
43 84.5 4.2 341 4 US-08-477-346-45 Sequence 45, Appl1
44 84.5 4.2 933 2 US-08-682-847-2 Sequence 2, Appl1
45 84.5 4.2 2890 4 US-09-413-814-67 Sequence 67, Appl1

ALIGNMENTS

RESULT 1
US-07-929-580B-2
; Sequence 2, Application US/07929580B
; Patent No. 5426181
; GENERAL INFORMATION:
; APPLICANT: Lee, Tae Ho
; APPLICANT: Lee, Gene W.
; APPLICANT: Vilcek, Jan
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
; TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bromdy and Neimark
; STREET: 419 Seventh Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION NUMBER: US/07929,580B
; FILING DATE: 19920814
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/640,492
; FILING DATE: 14-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Guy Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: LEE25\VLCEK-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-929-580B-2

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Best Local Similarity 100.0%; Pred. No. 1e-73;
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Db 61 IMLENSOMRERMILLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTSALDEL 120
QY 121 LQATDRAGRRRLARMEGAEAQRPEEAGRALAAVL 153
Db 121 LQATDRAGRRRLARMEGAEAQRPEEAGRALAAVL 153

RESULT 2
US-08-631-607-7
; Sequence 7, Application US/08631607
; Patent No. 5767252
; GENERAL INFORMATION:
; APPLICANT: Worley et al, Paul
; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,607
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/086001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-631-607-7

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Db 338 APWHPINPGVGLIGEDQD--TVGGRFDTAQFVGLSEFNINWDPVLFQAEIVNIANC-S 394
QY 357 CHIRGNIVGWGVTEIQPHGGA 377
Db 395 TNMPGNLIIPWVSNNDVFECCA 415

RESULT 3
US-08-631-607-2
; Sequence 2, Application US/08631607
; Patent No. 5767252
; GENERAL INFORMATION:
; APPLICANT: Worley et al, Paul
; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,607
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/086001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-631-607-2

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Query Match
14.6%; Score 294; DB 1; Length 430;

Best Local Similarity 26.0%; Pred. No. 5.7e-22;

Matches	99;	Conservative	53;	Mismatches	129;	Indels	100;	Gaps	14;
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Qy 113 I.TSAI.DEL.I.OATRDAGRRI.ARMEGAE-----AORPEEAGRAIAAV 152

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153 LEELROTTRADLH---AVOGWAARSWLPAGCETA---LDFPMRSKRI 191
QY
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Dh

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:20 ; Search time 28.4 Seconds
(without alignments)
993.730 Million cell updates/sec

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2007	100.0	381	20 AAY22803	Amino acid sequenc
2	1999	99.6	381	14 AAR42362	Pentaxin PTX3. Ho
3	1999	99.6	381	22 AAB90790	Human shear stress
4	788	39.3	178	13 AAR26181	TSG-14. Homo sapi
5	289.5	14.4	432	18 AAW31736	Neuronal activity-
6	289.5	14.4	432	22 AAB31178	Amino acid sequenc
7	278	13.9	502	22 AAU15114	Schizophrenia-asso
8	259.5	12.9	218	16 AAR74770	Limulus C-reactive
9	192	9.6	210	16 AAR74769	Female hamster pro
10	185.5	9.2	225	13 AAR29922	CRP. Homo sapiens
11	184.5	9.2	206	16 AAR74768	Human C-reactive p

12	184.5	9.2	206	18 AAW3405	Human C-reactive p
13	184.5	9.2	206	19 AAW40529	Human C-reactive p
14	184.5	9.2	206	20 AAW30582	Human C-reactive p
15	184.5	9.2	206	21 AAY76844	Human C-reactive p
16	167.5	8.3	204	16 AAR74763	Serum amyloid p c
17	152.5	7.6	203	22 AAB83050	Recombinant human
18	146.5	7.3	223	13 AAR29923	SAP. Homo sapiens
19	119	5.9	1316	22 AAB94754	Human protein sequ
20	115	5.7	689	22 AAU00713	Human novel G-prot
21	115	5.7	690	22 AAU00208	Human novel G-prot
22	115	5.7	690	22 AAU00717	Human novel G-prot
23	115	5.7	717	22 AAU00196	Human novel G-prot
24	115	5.7	718	22 AAU00192	Human novel G-prot
25	115	5.7	718	22 AAU00200	Human novel G-prot
26	115	5.7	1083	22 AAU00714	Human novel G-prot
27	115	5.7	1084	22 AAU00209	Human novel G-prot
28	115	5.7	1084	22 AAU00718	Human novel G-prot
29	115	5.7	1111	22 AAU00197	Human novel G-prot
30	115	5.7	1112	22 AAU00193	Human novel G-prot
31	115	5.7	1112	22 AAU00201	Human novel G-prot
32	115	5.7	1192	22 AAU00712	Human novel G-prot
33	115	5.7	1192	22 AAU00719	Human novel G-prot
34	115	5.7	1193	22 AAU00207	Human novel G-prot
35	115	5.7	1193	22 AAU00716	Human novel G-prot
36	115	5.7	1220	22 AAU00195	Human novel G-prot
37	115	5.7	1221	22 AAU00191	Human novel G-prot
38	115	5.7	1221	22 AAU00199	Human novel G-prot
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45	114	5.7	532	21 AAB42542	Human ORFX ORF2306

ALIGNMENTS

RESULT 1
AAV22803
ID AAY22803 standard; Protein; 381 AA.
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AC AAY22803;
DT 26-AUG-1999 (first entry)
XX
DE Amino acid sequence of human long pentraxin (PTX3).
XX Human; long pentraxin; PTX3; gene therapy; cancer; infectious disease;
KW inflammatory disease; tumour disease; anticancer.
XX Homo sapiens.
XX WO9932516-A2.
XX PD 01-JUL-1999.
XX PF 16-DEC-1998; 98WO-IT00364.
XX PR 19-DEC-1997; 97IT-RM00796.
XX (SIC) SIGMA-TAU IND FARM RIUNITE SPA.
PA Bottazzi B, Introna M, Mantovani A, Vecchi A;
PI WPI; 1999-405159/34.
DR N-PSDB; AAX81675.
XX New pharmaceutical compositions containing pentraxin (PTX3), useful
PT for treating infectious and inflammatory diseases or tumours
XX Disclosure: Page 22-24; 26pp; English.
PS

